



#15

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/319,156
Source: 1648
Date Processed by STIC: 2/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

09/319,156

ad

Application No.: _____

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

#13

1648

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/319,156

TIME: 12:42:40

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

see
P. 5Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: PARANHOS-BACCALA, Glaucia
 4 KOMURIAN-PRADEL, Florence
 5 BEDIN, Frederic
 6 SODOYER, Mireille
 7 OTT, Catherine
 8 MALLET, Francois
 9 PERRON, Herve
 10 MANDRAND, Bernard
 12 <120> TITLE OF INVENTION: RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN
 PARTICULAR,
 13 ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC,
 14 PROPHYLACTIC AND THERAPEUTIC USES
 16 <130> FILE REFERENCE: 103514
 18 <140> CURRENT APPLICATION NUMBER: US/09/319,156
 19 <141> CURRENT FILING DATE: 1999-11-02
 21 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01460
 22 <151> PRIOR FILING DATE: 1998-07-07
 24 <150> PRIOR APPLICATION NUMBER: FR/97/08816
 25 <151> PRIOR FILING DATE: 1997-07-07
 27 <160> NUMBER OF SEQ ID NOS: 45
 29 <170> SOFTWARE: PatentIn version 3.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 34
 33 <212> TYPE: DNA
 34 <213> ORGANISM: MSRV
 36 <400> SEQUENCE: 1
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 41 <211> LENGTH: 30
 42 <212> TYPE: DNA
 43 <213> ORGANISM: MSRV
 45 <400> SEQUENCE: 2
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 50 <211> LENGTH: 30
 51 <212> TYPE: DNA
 52 <213> ORGANISM: MSRV
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 59 <211> LENGTH: 310
 60 <212> TYPE: DNA
 61 <213> ORGANISM: MSRV
 63 <400> SEQUENCE: 4
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 66 agcaggaaaa atagaatagg aaacctcaca aggacatact ttcctcccct ccagatggct 120
 68 agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180
 70 ccttcaccaa accttcact taggcattga tagcacccat cagatggcca aattattatt 240

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Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

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74 aagaaataat                                     310
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79 <212> TYPE: PRT
80 <213> ORGANISM: MSRV
82 <220> FEATURE:
83 <221> NAME/KEY: misc_feature
84 <222> LOCATION: (26)..(26)
85 <223> OTHER INFORMATION: Xaa = any amino acid
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90 Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys
91 1 5 10 15
93 Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
94 20 25 30
96 Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
97 35 40 45
99 Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
100 50 55 60
102 Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
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108 Glu Val Cys Gln Arg Asn Asn
109 100
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114 <213> ORGANISM: MSRV
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121 ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccag      180
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125 catcagccaa cctccccaac agcacttggg ttttctgtt gagagggggg actgagagac      300
127 aggactagct ggatttcta ggccaacgaa gaatccctaa gcctagctgg gaaggtgact      360
129 gcatccacct ctaaaccatgg ggcttgcaac ttagctcaca cccgaccaat cagagagctc      420
131 actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg      480
133 agagcacagc gggagggaca aggatcggga tataaaccca ggcattcgag ccggcaacgg      540
135 caacccccct tgggtccctt ccctttgtat gggcgctctg ttttcactct atttcactct      600
137 attaaatctt gcaactgaaa aaaaaaaaaa aaaaa      635
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 77
142 <212> TYPE: PRT
143 <213> ORGANISM: MSRV
145 <400> SEQUENCE: 7
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148 1 5 10 15
150 Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser

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RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/319,156

TIME: 12:42:40

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

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151          20          25          30
153 Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
154          35          40          45
156 Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
157          50          55          60
159 Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
160 65          70          75
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163 <211> LENGTH: 32
164 <212> TYPE: DNA
165 <213> ORGANISM: MSRV
167 <400> SEQUENCE: 8
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181 acgcggtctt ctggaaatat tgatgcccc aactgtctata actctgccac tctttgcatg 180
183 accttccactg cccacaccca tatgccccgc aactgtctata actctgccac tctttgcatg 240
185 catgcaaata ctcatatttg gacagggaaa atgattaatc ctagtgtgctc tggaggactt 300
187 ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg ggttggaatt 360
189 caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat 420
191 agcaccctta gccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480
193 catactgcc tgggtgagct atttaatacc accctcactc ggtccatga ggtctcagcc 540
195 caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600
197 cctgttctctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta 660
199 ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720
201 agcaatac tagacacaac cagctcccaa tgcatacagg gggtaacacc tcccacacga 780
203 atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg 840
205 aatggctctt cagaatctat gtgttctctc tcattcttag tgccccctat gaccatctac 900
207 actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtaccatt 960
209 ctctcttttg ttatcagagc aggagtgcga ggcagactag gtactggcat tggcagtatc 1020
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213 gtcactgact ccttggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140
215 caaaatcgaa gagctttaga cttgctaacc gccaaaagag ggggaacctg tttattttta 1200
217 ggagaagaac gctgttatta tgttaataca tccagaattg tcaactgagaa agttaagaa 1260
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221 ctacagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaattattg 1380
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229 <211> LENGTH: 493
230 <212> TYPE: PRT
231 <213> ORGANISM: MSRV
233 <220> FEATURE:
234 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/319,156

TIME: 12:42:40

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

235 <222> LOCATION: (39)..(39)

236 <223> OTHER INFORMATION: Xaa = any amino acid

239 <400> SEQUENCE: 10

241 Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro

242 1 5 10 15

244 Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser

245 20 25 30

247 Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp

248 35 40 45

250 Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala

251 50 55 60

253 His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met

254 65 70 75 80

256 His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys

257 85 90 95

259 Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr

260 100 105 110

262 Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln

263 115 120 125

265 Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser

266 130 135 140

268 Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr

269 145 150 155 160

271 His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His

272 165 170 175

274 Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu

275 180 185 190

277 His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn

278 195 200 205

280 Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val

281 210 215 220

283 Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe

284 225 230 235 240

286 Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr

287 245 250 255

289 Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys

290 260 265 270

292 Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys

293 275 280 285

295 Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp

296 290 295 300

298 Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile

299 305 310 315 320

301 Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly

302 325 330 335

304 Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln

305 340 345 350

307 Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu

308 355 360 365

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Input Set : A:\es.txt
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310 Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
311      370                      375                      380
313 Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
314 385                      390                      395                      400
316 Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
317                      405                      410                      415
319 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
320                      420                      425                      430
322 Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
323                      435                      440                      445
325 Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Phe
326                      450                      455                      460
328 Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
329 465                      470                      475                      480
331 Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
332                      485                      490

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334 <210> SEQ ID NO: 11

335 <211> LENGTH: 32

336 <212> TYPE: DNA

337 <213> ORGANISM: MSRV

339 <400> SEQUENCE: 11

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32

343 <210> SEQ ID NO: 12

344 <211> LENGTH: 1329

345 <212> TYPE: DNA

346 <213> ORGANISM: MSRV

348 <220> FEATURE:

349 <221> NAME/KEY: misc_feature

350 <222> LOCATION: (1232)..(1232)

351 <223> OTHER INFORMATION: n = a, g, c or t/u

354 <400> SEQUENCE: 12

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355 tcaaaatcga agagcttttag acttgctaac cgccaaaaga gggggaacct gtttattttt 60
357 aggggaagaa tgctgttagt atgttaatca atctggaatc attactgaga aagttaaaga 120
359 aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct 180
361 cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt 240
363 tttactcttc tttggaccct gtatcttcaa cttccttggt aagtgtgtct cttccagaat 300
365 tgaagctgta aagctacaaa tagttcttca aatggaaccc cagatgcagt ccatgactaa 360
367 aatctaccgt ggaccctctg accggcctgc tagactatgc tctgatgta atgacattga 420
369 agtcaccct cccgaggaaa tctcaactgc acaaccctca ctacactcca attcagtagg 480
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377 accaatcaga gagctcacta aaatgctaata caggcaaaaa caggaggtaa agcaatagcc 720
379 aatcatctat tgcttgagag cacagcggga aggacaagga ttgggatata aactcaggca 780
381 ttcaagccag caacagcaac cccctttggg tcccctccca ttgtatggga gctctgtttt 840
383 cactctattt cactctatta aatcatgcaa ctgcactctt ctggtccgtg ttttttatgg 900
385 ctcaagctga gcttttggc gccatccacc actgctgttt gccaccgtca cagaccgct 960
387 gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt 1020
389 acccattgcc actcccgatc aggctaaagg cttgccattg ttctgcatg gctaagtgcc 1080

```

what about n's at locations 594 and 602?

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/319,156

DATE: 07/25/2001

TIME: 12:42:41

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40